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FIG. 1

R35464	GGCCGGGTCG TTTCTCGCCT GGCTGGGATC GCTGCTCCTC TCTGGGGTCC	50
ORF	P G R F S P G W D R C S S L G S	16
R35464	TGGCCGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTGAA	100
ORF	W P A D R E R S I H D F C L V S K	33
R35464	GGTGGTGGGC AGATTCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA	150
ORF	V V G R F R A S M P R W W Y N V T	50
R35464	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC	200
ORF	D G S C Q L F V Y G G C D G N S	66
R35464	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC	250
ORF	N N Y L T K E E C L K K C A T V T	83
R35464	AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT	300
ORF	E N A T G D L A T S R N A A D S S	100
R35464	CTGTCCCAAG TGCTCCAGA AGGCAGGATT CTTGAAGACC ACTTCAGCGA	350
ORF	V P S A P R R Q D S * R P L Q R	116
R35464	TATGTTTCAA NTATTGNAAG AATAATTGCA CCGNCAACGN ATT-----	393
ORF	Y V S * I * R I I A P * T *	130

KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO:12)

ORF = EST R35464 Open Reading Frame Translation (SEQ ID NO: 13)



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FIG. 2

R74593	GCAATAATTA CCTGACCAAG GAGGAGTGCC TCAAGAAATG TGCCACTGTC	50
ORF	Q * L P D Q G G V P Q E M C H C H	17
R74593	ACAGAGAATG CCACGGGTGA CCTGGCCACC AGCAGGAATG CAGCGGATTC	100
ORF	R E C H G * P G H Q Q E C S G F	33
R74593	CTCTGTCCCA AGTCTCCCAG AAGGCAGGAT TCTGAAGACC ACTCCAGCGA	150
ORF	L C P K S P R R Q D S E D H S S D	50
R74593	TATGTTCAAC TATGAAGAAT ACTGCACCGC CAACGCAGTC ACTGGGCCTT	200
ORF	M F N Y E E Y C T A N A V T G P C	67
R74593	GCCGTGCATC CTTCCCACGC TGGTACTTTG ACGTGGAGAG GAACTCCTGC	250
ORF	R A S F P R W Y F D V E R N S C	83
R74593	AATAACTTCA TCTATGGAGG CTGCCGGGGC AATAAGAACA GCTACCGCTC	300
ORF	N N F I Y G G C R G N K N S Y R S	100
R74593	TGAGGAGGCC TGCATGCTCC GCTGCTTCCG CCAGCAGGAG AATCCTCCCC	350
ORF	E E A C M L R C F R Q Q E N P P L	117
R74593	TGCCCCTTGG CTCAAAGGTG GTGGTTCTGG CCGGGGCTGT TTCGTGATGG	400
ORF	P L G S K V V V L A G A V S * W	133
R74593	TGTTGATCCT TTTCTGGGG AGCNTCCATG GTCTTACTGA TTCCGGGTGG	450
ORF	C * S F S W G A S M V L L I P G G	150
R74593	CAAGGAGGAA CCAGGAGCGT GCCCTGCGGA NCGTCTGGAG CTTCCGAGAT	500
ORF	K E E P G A C P A X R L E L R R *	167
R74593	GACAAGGGNT	510
ORF	Q G	169

KEY

R74593 = Nucleic acid sequence of EST R74593 (SEQ ID NO: 14)

ORF = EST R74593 Open Reading Frame Translation (SEQ ID NO: 15)



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FIG. 3

R35464	GGCCGGGTCGT TTCTCGCCTG GCTGGGA-TC GCTGCTCCTC TCTGGGGTCC	50
N39798	TGGGANTC GCTGCTCCTC TCTGGGGTCC	28
H94519	GCNGCG-CGT TNNTCGCNT- GCTGGGA-TC GCTGCACCTC TCTGGGGTCC	47
R74593 corr.	-----	
Consensus	GGCCGGGTCGT TTCTCGCCTG GCTGGGA-TC GCTGCTCCTC TCTGGGGTCC	50
Translation	A G S F L A W L G S L L L S G V	-3
R35464	TGGCCGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTGCGAA	100
N39798	TGG-CGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTGCGAA	77
H94519	NGG-CGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTGCGAA	96
R74593 corr.	-----	
Consensus	TGG-CGGCCG ACCGAGAACG CAGCATCCAC GACTTCTGCC TGGTGTGCGAA	99
Translation	L A A D R E R S I H D F C L V S K	15
R35464	GGTGGTGGGC AGATTCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA	150
N39798	GGTGGTGGGC AGATGCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA	127
H94519	GGTGGTGGGC AGATGCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA	146
R74593 corr.	-----	
Consensus	GGTGGTGGGC AGATGCCGGG CCTCCATGCC TAGGTGGTGG TACAATGTCA	149
Translation	V V G R C R A S M P R W W Y N V T	32
R35464	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC	200
N39798	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC	177
H94519	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC	196
R74593 corr.	-----	
Consensus	CTGACGGATC CTGCCAGCTG TTTGTGTATG GGGGCTGTGA CGGAAACAGC	199
Translation	D G S C Q L F V Y G G C D G N S	48
R35464	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC	250
N39798	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC	227
H94519	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC	246
R74593 corr.	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC	52
Consensus	AATAATTACC TGACCAAGGA GGAGTGCCTC AAGAAATGTG CCACTGTCAC	249
Translation	N N Y L T K E E C L K K C A T V T	65
R35464	AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT	300
N39798	AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT	277
H94519	AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT	296
R74593 corr.	AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT	102
Consensus	AGAGAATGCC ACGGGTGACC TGGCCACCAG CAGGAATGCA GCGGATTCCT	299
Translation	E N A T G D L A T S R N A A D S S	82
R35464	CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CTGAAGACC ACTTCAGCGA	350
N39798	CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAGCGA	326
H94519	CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAGCGA	345
R74593 corr.	CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAGCGA	151
Consensus	CTGTCCCAAG TGCTCCCAGA AGGCAGGATT CT-GAAGACC ACTCCAGCGA	348
Translation	V P S A P R R Q D S E D H S S D	98



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FIG. 3 (Cont.)

R35464	TATGTTTCAA	NTATTGNAAG	AATAATTGCA	CCGNCAACGN	ATT-----	393
N39798	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	372
H94519	TATGTT-CAA	CTA-TG-AAG	AATACTGGCA	CCGCCAACGC	ATTCACTGGG	392
R74593 corr.	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	197
Consensus	TATGTT-CAA	CTA-TG-AAG	AATACT-GCA	CCGCCAACGC	AGTCACTGGG	394
Translation	M	F	N	Y	E E Y C T A N A V T G	113
R35464	-----	-----	-----	-----	-----	
N39798	CCTTGC-GTG	GAATCCTTTC	CCACGCTGGN	AATTNGACG	TTGAGAAGGA	421
H94519	CCT-GC-GTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GNCG	-----	427
R74593 corr.	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	243
Consensus	CCTTGCCGTG	-CATCCTT-C	CCACGCTGGT	ACTTT-GACG	TGGAGA-GGA	440
Translation	P	C	R	A	S F P R W Y F D V E R N	129
R35464	-----	-----	-----	-----	-----	
N39798	AC-----	-----	-----	-----	-----	423
H94519	-----	-----	-----	-----	-----	
R74593 corr.	ACTCCTGCAA	TAACCTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	293
Consensus	ACTCCTGCAA	TAACCTTCATC	TATGGAGGCT	GCCGGGGCAA	TAAGAACAGC	490
Translation	S	C	N	N	F I Y G G C R G N K N S	145
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	343
Consensus	TACCGCTCTG	AGGAGGCCTG	CATGCTCCGC	TGCTTCCGCC	AGCAGGAGAA	540
Translation	Y	R	S	E	E A C M L R C F R Q Q E N	162
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCCTCCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	393
Consensus	TCCTCCCCTG	CCCCTTGGCT	CAAAGGTGGT	GGTTCTGGCC	GGGGCTGTTT	590
Translation	P	P	L	P	L G S K V V V L A G A V S	179
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	443
Consensus	CGTGATGGTG	TTGATCCTTT	TCCTGGGGAG	CNTCCATGGT	CTTACTGATT	640
Translation	*	W C	* S F	S W G A	S M V L L I	195
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	GTCTGGAGCT	493
Consensus	CCGGGTGGCA	AGGAGGAACC	AGGAGCGTGC	CCTGCGGANC	<u>GTCTGGAGCT</u>	690
Translation	P	G	G	K	E E P G A C P A * R L E L	212
R35464	-----	-----	-----	-----	-----	
N39798	-----	-----	-----	-----	-----	
H94519	-----	-----	-----	-----	-----	
R74593 corr.	TCGGAGATGA	CAAGGGNT				511
Consensus	<u>TCGGAGATGA</u>	CAAGGGNT				708
Translation	R	R	*	Q	G	217



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FIG. 3 (Cont.)

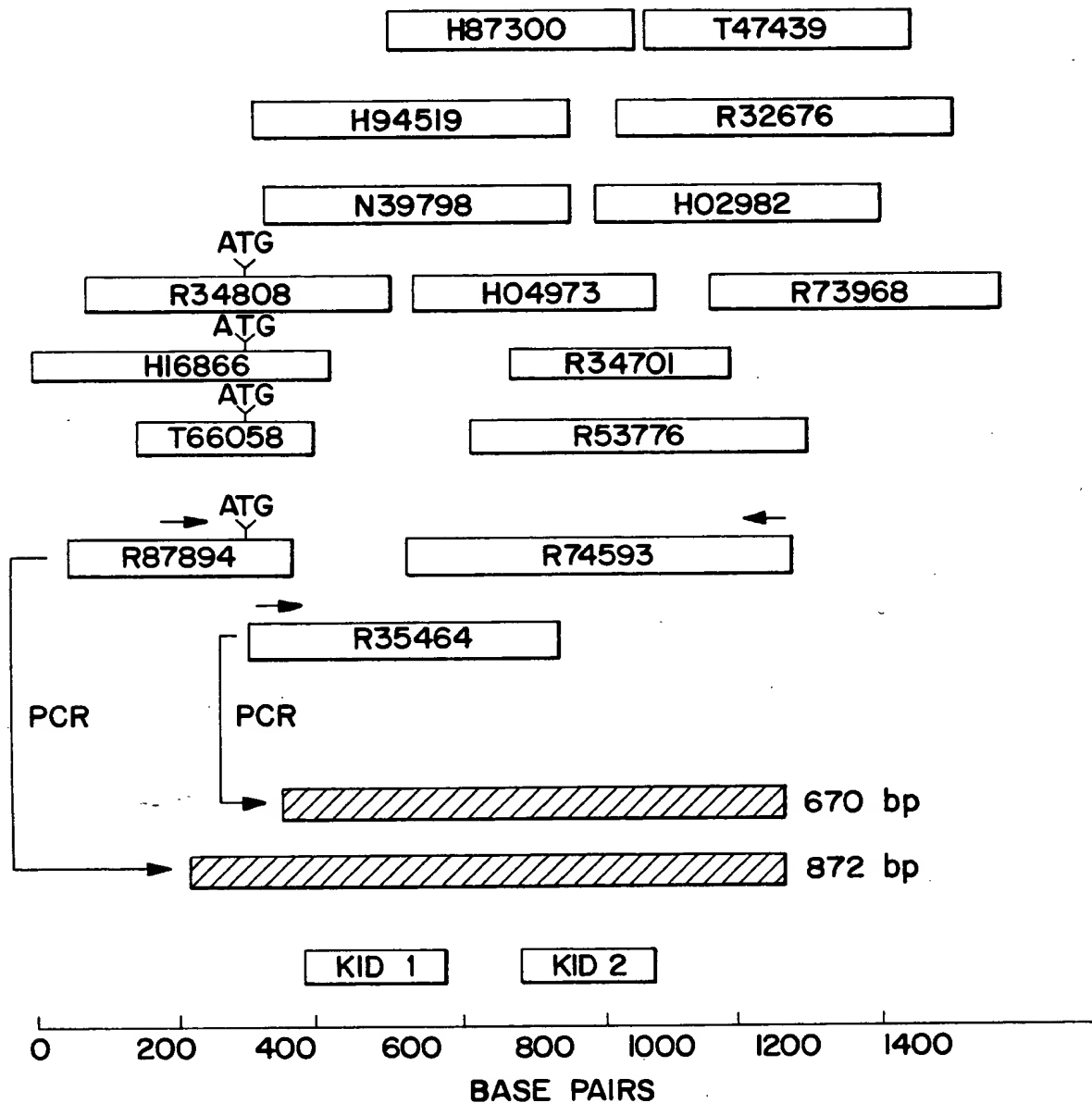
KEY

R35464 = Nucleic acid sequence of EST R35464 (SEQ ID NO.: 12)
N39798 = Nucleic acid sequence of EST N39798 (SEQ ID NO.: 17)
H94519 = Nucleic acid sequence of EST H94519 (SEQ ID NO.: 16)
R74593 corr = Corrected version of (SEQ ID NO.: 14) G at b.p. 114
Consensus = Nucleic acid sequence for human bikunin (SEQ ID NO. 9)
Translation = Amino acid Translation of Consensus (SEQ ID NO.: 10)



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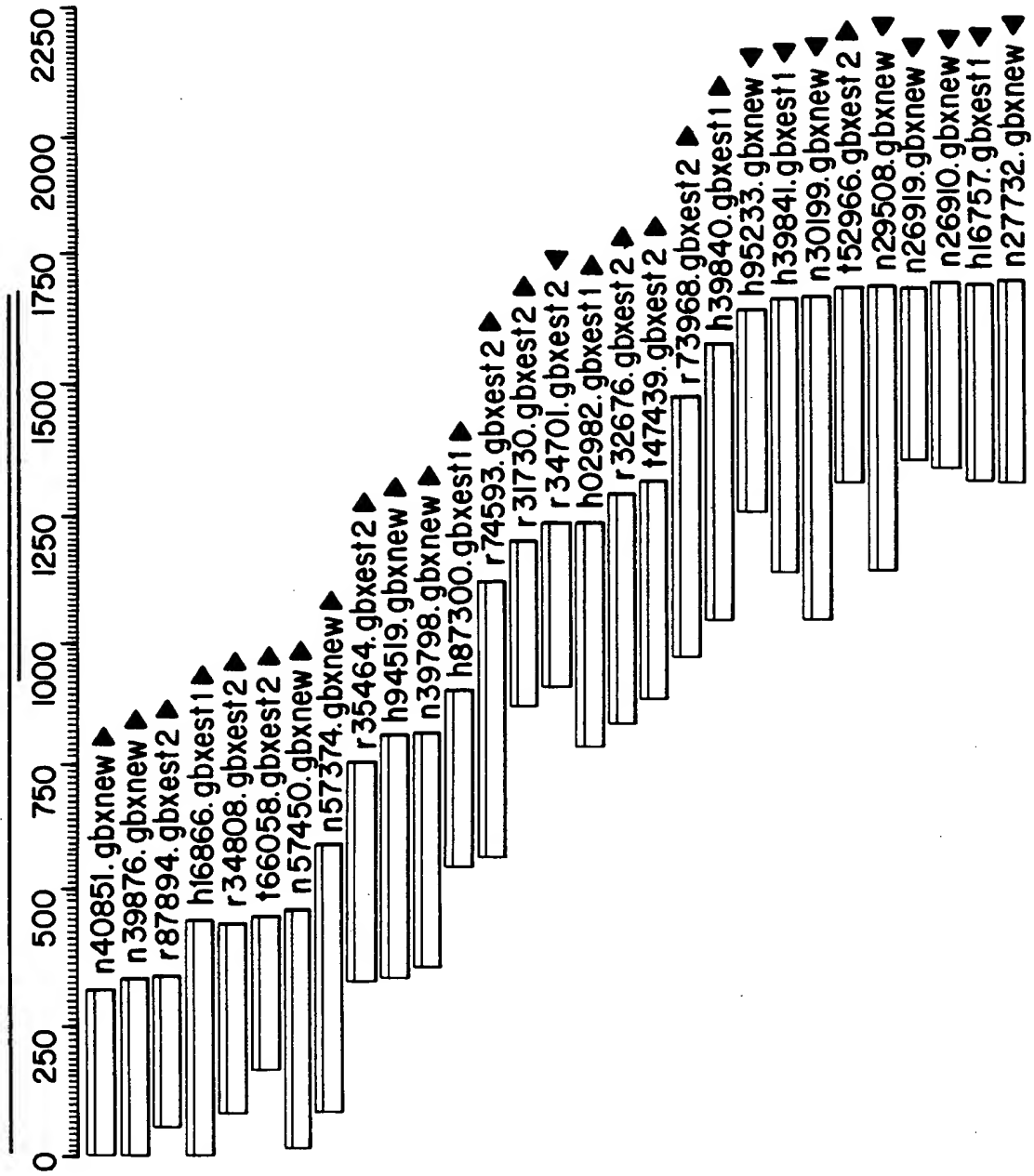
FIG. 4A

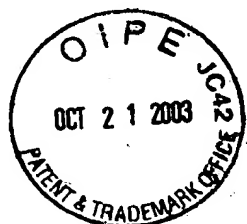




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FIG. 4B





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FIG. 4C

	1				50
BikuninGCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N40851GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
N39876GCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCGGCT	CTGAACGCGT
R87894				
H16866GGCGA	CCTCCGCGCG	TTGGGAGGTG	TAGCGCG. CT	CTGAACGGGN
R34808				
T66058				
N57450T	TAGCGCGGCT	CTGAACGCNA
N57374				
R35464				
H94519				
N39798				
H87300				
R74593				
R31730				
R34701				
H02982				
R32676				
T47439				
R73968				
H39840				
H95233				
H39841				
N30199				
T52966				
N29508				
N26919				
N26910				
H16757				
N27732				



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FIG. 4C (Cont.)

	51				100
Bikunin	GNA GGGCCG	TTGAGTGTCTG	CAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
N40851	NGAGNNGGCCG	TTGAGTGTCTG	CAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
N39876	GCA.GGGCCG	TTGAGTGTCTG	CAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
R87894	TTGAGTGTNG	NAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
H16866	..ANGGGCCG	TTGAGTGTCTG	CAGGCGGC.A	GGGCN.GAGT	GAGGAGCAGA
R34808G	GAGGAGCAGA
T66058
N57450	GAAGNNGGCCG	TTGAGTGTCTG	CAGGCGGCGA	GGGCGCGAGT	GAGGAGCAGA
N57374AGA
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	101					150
Bikunin	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	GTCCCCACAC	TGAAGGTCCG
N40851	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	GTCCCCACAC	TGAAGGTCCG
N39876	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	NTCCCCACAC	TGAAGGTCCG
R87894	CCCAGGCATC	GCGCGCCGAG	AAGGCCGGGC		GTCCCCACAC	TGAAGGTCCG
H16866	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	GTCCCCACAC	TGAAGGTCCG
R34808	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	GTCCCCACAC	TGAAGGTCCG
T66058
N57450	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	GTCCCCACAC	TGAAGGTCCG
N57374	CCCAGGCATC	GCGCGCCGAG	AAGNC	GGGC	GTCCCCACAC	TGAAGGTCCG
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	151				200
Bikunin	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N40851	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N39876	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
R87894	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
H16866	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACG.T	CCCGGAGCN.
R34808	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
T66058GGACCCT	CCCGGAGCGT
N57450	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
N57374	GAAAGGCGAC	TTCCGGGGGC	TTTGGCACCT	GGCGGACCCT	CCCGGAGCGT
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	201				250
Bikunin	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	.AGGGGCTTC
N40851	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTNTG	.AGGGGCTTC
N39876	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	.AGGGGCTTC
R87894	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	.AGGGGCTTC
H16866	.GGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	.AGGGGCTTC
R34808	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTNTG	GAGGGGCTTC
T66058	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	.GTGCGTGTG	NAGGGGCTTC
N57450	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	.AGGGGCTTC
N57374	CGGCACCTGA	ACGCGAGGCG	CTCCATTGCG	CGTGCGTTTG	.AGGGGCTTC
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	251				300
Bikunin	CCGCACCT G	ATCGCGAGAC	CCCAACGGCT	GGTGG CGTC	GC TG CGCG
N40851	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GCCTG.CGCG
N39876	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GCCTG.CGCG
R87894	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTNG.CGTC	GC.TN.CGCG
H16866	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTNG.CGTC	GC.TGGCGCG
R34808	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGGGCGTC	GC.TG.CGCG
T66058	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GC.TG.CGCG
N57450	CCGCACCT.G	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GCCTG.CGCG
N57374	CCGGAACCTG	ATCGCGAGAC	CCCAACGGCT	GGTGG.CGTC	GC.TG.CGCG
R35464
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	301				350
Bikunin	TC TCGGCTG	AGCT GGCCA	TGGCGCANT	GTTGC GGGC	T GAGGC GG
N40851	TC.TCGGCTG	AGCT.GGNCA	TGTCG		
N39876	TC.TCGGCTG	AGCT.GGCCA	TGGCGCACT.	G.TGCGGNGC	T.GAGGC.G
R87894	TC.TCGGCTG	AGCTTGGCCA	TGGCGCANT.	GTTNC.GGGC	T.NAGGC.GG
H16866	TTCTCGGCTG	AGCT.GGCCA	TGGCGCANT.	GTTGC.GNGC	T.GAGGC.GG
R34808	TCTTCGGCTG	AGCTGGGCCA	TGGCGCANTT	GTTGC.GGGC	T.GAGGC.GG
T66058	TC.TCGGCTG	AGCT.GGCCA	TGGCGCANT.	GTTGC.GNGC	T.GAGGC.GG
N57450	TC.TCGGCTG	AGCT.GGCCA	TGGCGCANT.	GGTGC.GGGC	TTGAGGC.GG
N57374	TCCTCGGCTG	AGCT.GGCCA	TGGCGCANT.	GGTGCCGNGC	T.GAGGCCGG
R35464GGCCGG
H94519
N39798
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	351				400
Bikunin	AC GG CG	TTTCTCG	CC TGCTGGG	A TCGCT GC	T CCTCTCT
R87894	ACG.				
H16866	AC..CGNCGT	TTTTCTTCG.	CCTTGCTGGG	ATTCGCTTGC	TTCCNTNTCTG
R34808	ACGCGGNCG.	.TTTTTTTCGN	CCTTGCTGGG	ATTCG.TTG.	TTNCTCTCTN
T66058	...CGNCG.	.TTTTCTCG.	CC.TGCTGGG	A.TCGCT.GC	T.CCTCTCT.
N57450	ANN.NGCCG.	.TTTCTCG.	CC.TGCTGGG	A.TCGCT.GC	T.CCTCTCT.
N57374	AG..GGCCGG	.TTTCTCG.	CCTTGCTGGG	A.TCGCT.GC	T.CCTCTCTG
R35464GTCG.	.TTTCTCG.	CCTGGCTGGG	A.TCGCT.GC	T.CCTCTCT.
H94519	.GCNGCGCG.	.TTNNTCG.	CN.TGCTGGG	A.TCGCT.GC	A.CCTCTCT.
N39798CTGGG	ANTCGCT.GC	T.CCTCTCT.
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	451					500
Bikunin	GCCTGGTGT	CGAAGGT GG	TGGGCAGATG	CCGGG	CCTC	CATGCCTA G
H16866	GCC					
T66058	TCCTGGTGTT	CGAAGG				
N57450	GCCTGGTGT.	CGAAGGT.GG	TGGGCAG			
N57374	GCCTGGTGTT	CGAAAGTTGG	TGGGCANATT	CCGGGGCCTT	CATGNCTAAG	
R35464	GCCTGGTGT.	CGAAGGT.GG	TGGGCAGATT	CCGGG.CCTC	CATGCCTA.G	
H94519	GCCTGGTGT.	CGAAGGT.GG	TGGGCAGATG	CCGGG.CCTC	CATGCCTA.G	
N39798	GCCTGGTGT.	CGAAGGT.GG	TGGGCAGATG	CCGGG.CCTC	CATGCCTA.G	
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
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FIG. 4C (Cont.)

	501				550
Bikunin	G TGGT GGT	ACAATGTCAC	TGACGGATCC	TGCCAGCTGT	TTGTGT ATG
N57374	GTTGGTTGGT	ANAATGTNAA	TTAANGATTG	TTGCAACTGT	TTGTGTNATT
R35464	G.TGGT.GGT	ACAATGTCAC	TGACGGATCC	TGCCAGCTGT	TTGTGT.ATG
H94519	G.TGGT.GGT	ACAATGTCAC	TGACGGATCC	TGCCAGCTGT	TTGTGT.ATG
N39798	G.TGGT.GGT	ACAATGTCAC	TGACGGATCC	TGCCAGCTGT	TTGTGT.ATG
H87300
R74593
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732
	551				600
Bikunin	GGGGCTGTGA	CGGAAACA	GCAATAATTA	CCTGACCAAG	GA GGAGTGC
N57374	GGGGCTNTTA	AACGGAAANA	.CAATAATNA	CCTGACCAAA	GAAGNAAT..
R35464	GGGGCTGTGA	..CGGAAACA	GCAATAATTA	CCTGACCAAG	GA.GGAGTGC
H94519	GGGGCTGTGA	..CGGAAACA	GCAATAATTA	CCTGACCAAG	GA.GGAGTGC
N39798	GGGGCTGTGA	..CGGAAACA	GCAATAATTA	CCTGACCAAG	GA.GGAGTGC
H87300	GATTCGGCAC	AGGGGAAACA	GCAATAATTA	CCTGACCAAG	GA.GGAGTNC
R74593	GCAATAATTA	CCTGACCAAG	GA.GGAGTGC
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	601				650
Bikunin	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
R35464	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
H94519	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
N39798	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
H87300	CTCAAGAAAT	GTNCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
R74593	CTCAAGAAAT	GTGCCACTGT	CACAGAGAAT	GCCACGGGTG	ACCTGGCCAC
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732
	651				700
Bikunin	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
R35464	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
H94519	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
N39798	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
H87300	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGTGCTCCC	AGAAGGCAGG
R74593	CAGCAGGAAT	GCAGCGGATT	CCTCTGTCCC	AAGT . CTCCC	AGAAGGCAGG
R31730
R34701
H02982
R32676
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	701						750
Bikunin	ATTCT GAAG ACCACTCCAG CGATATGTT CAACTAT G AAGAATACTG						
R35464	ATTCTTGAAG ACCACTTCAG CGATATGTTT CAANTATTGN AAGAATAATT						
H94519	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG						
N39798	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG						
H87300	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG						
R74593	ATTCT.GAAG ACCACTCCAG CGATATGTT. CAACTAT..G AAGAATACTG						
R31730						
R34701						
H02982						
R32676						
T47439						
R73968						
H39840						
H95233						
H39841						
N30199						
T52966						
N29508						
N26919						
N26910						
H16757						
N27732						
	751						800
Bikunin	CACCGCCAA CGCAGT CAC TGGGCC TTG CCGTG CAT CCTT CCCAC						
R35464	GCACCGNCAA CGNATT						
H94519	GCACCGCCAA CGCATT.CAC TGGGCC..TG C.GTG.CAT. CCTT.CCCAC						
N39798	.CACCGCCAA CGCAGT.CAC TGGGGCCTTG C.GTGGAAAT. CCTTTCCCAC						
H87300	.CACCGCCAA CGCAGTNCAC TGGGCC.TTG C.GTGGCATN CCTT.CCCAC						
R74593	.CACCGCCAA CGCAGT.CAC TGGGCC.TTG CCGTG.CAT. CCTT.CCCAC						
R31730						
R34701						
H02982						
R32676						
T47439						
R73968						
H39840						
H95233						
H39841						
N30199						
T52966						
N29508						
N26919						
N26910						
H16757						
N27732						



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FIG. 4C (Cont.)

	801					850
Bikunin	GCTGGTACTT	T	GACGTGGA	GA	GGAAGCTC	CTG CAATAA CTTTCATCTAT
H94519	GCTGGTACTT	T	GNCGT			
N39798	GCTGGNAATT	TNGACGTTGA	GAAGGAAC			
H87300	GCTNGTACTT	T	GACGTGGA	GA	GGAAGCTC	CTGGCAATAA CTTTCATCTAT
R74593	GCTGGTACTT	T	GACGTGGA	GA	GGAAGCTC	CTG.CAATAA CTTTCATCTAT
R31730
R34701
H02982	GA	GA	GGAAGCTC	CTG.CAATAA CTTTCATCTAT
R32676	G ATTC..GGAA
T47439
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732
	851					900
Bikunin	GGAGGCT GC	CGGGGCAAT	AAGAACAG C	TACCGCTC T	GAGGAGGCCT	
H87300	GGAGGCTTGC	CGGGGCAATN	AAGAACAGNT	TACCGCTCTT	TAGGAGGCCT	
R74593	GGAGGCT.GC	CGGGGCAAT.	AAGAACAG.C	TACCGCTC.T	GAGGAGGCCT	
R31730	G.C	TACCGCTC.T	GAGGAGGCCT
R34701
H02982	GGNGGCT.GC	CGGGG.AAT.	AAGAACA.NC	TACCGCTC.T	GAGGAGGCCT	
R32676	CGAGGA..GC	CGGGGCAAT.	AAGAACAG.C	TACCGCTC.T	GAGGAGGCCT	
T47439	NGGCCT
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	901	950
Bikunin	GCA TGCTC CGCTGCTTCC GC	CA GCAGGA
H87300	.GCA.T....	
R74593	.GCA.TGCTC CGCTGCTTCC GC.....	.CA.GCAGGA
R31730	.GCA.TGCTC CGCTGCTTCC GC.....	.CA.GCAGGA
R34701TTCC GC.....	.CAAGCAGGA
H02982	.GCG.TGCTC CGCTGCTTCC GCTGTGTGTT CTCTTCCAGG	CCA.GCAGGA
R32676	.GCA.TGCTC CGCTGCTTCC GC.....	.CA.GCAGGA
T47439	TGCAGTGCTC CGCTGCTTCC GC.....	.CA.GCAGGA
R73968
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732

	951	1000
Bikunin	GAA TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG CGGGGC
R74593	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGGCGGGGC
R31730	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R34701	AAANTCCTCC CCTCCCCCTT GGCTCAAAGG TGGTGGTTC	TGG.CGGGGC
H02982	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R32676	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
T47439	GAA.TCCTCC CCTGCCCCCTT GGCTCAAAGG TGGTGGTTC.	TGG.CGGGGC
R73968CGGGGC
H39840
H95233
H39841
N30199
T52966
N29508
N26919
N26910
H16757
N27732



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FIG. 4C (Cont.)

	1001					1050
Bikunin	TGTT CGTGA	TGGTGTGAT	CC T CTTCC	TGGG AGCCT	CC ATGGTC	
R74593	TGTTTCGTGA	TGGTGTGAT	CCTT..TTCC	TGGGGAGCNT	CC.ATGGTCT	
R31730	TGTT.CGTGA	TGGTGTGAT	CC.T.CTTCC	TGGGGAGCCT	CC.ATGGTC.	
R34701	TGTT.CGTGA	TGGTGTGAT	CCCTCCTTCC	CGGG.AGCCT	CCCATGGTCC	
H02982	TGTT.CGTGA	TGGTGTGAT	CC.T.CTTCC	TGGG.AGCCT	CC.ATGGTN.	
R32676	TGTT.CGTGA	TGGTGTGAT	CC.T.CTTCC	TGGG.AGCCT	CC.ATGGTC.	
T47439	TGTT.CGTGA	TGGTGTGAT	CC.T.CTTCC	TGGG.AGCCT	CC.ATGGTC.	
R73968	TGTT.CGTGA	TGGTGTGAT	CC.T.CTTCC	TGGG.AGCCT	CC.ATGGTC.	
H39840	
H95233	
H39841	
N30199	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	
	1051					1100
Bikunin	TACC TGAT	CCGGGTGGCA	CGGAGG AAC	C AGG AGCG	TGCCCTGCGC	
R74593	TAC..TGATT	CCGGGTGGCA	AGGAGG.AAC	C.AGG.AGCG	TGCCCTGCGG	
R31730	TACC.TGAT.	CCGGGTGGCA	CGGAGGGAAC	C.AGGGAGCG	TGCCCTGCGC	
R34701	TACCCTGAT.	CCGGGTGGCA	CGGAGG.AAC	CCAGG.ANCG	TGCCCTGCGC	
H02982	TACC.TGAT.	CCGGGTNGCA	CGGAGG.AAC	C.AGGGAGCG	TGCCCTGCGN	
R32676	TACC.TGAT.	CCGGGTGGCA	CGGAGG.AAC	C.AGGGAGCG	TGCCCTGCGC	
T47439	TACC.TGAT.	CCGGGTNGCA	CGGAGG.AAC	C.AGG.AGCG	TGCCCTGCGC	
R73968	TACC.TGAT.	CCGGGTGGCA	CGGAGG.AAC	C.AGG.AGCG	TGCCCTGCGC	
H39840GGG.AAC	C.AGG.AGCG	TGCCCTGCGC	
H95233	
H39841	
N30199GAGGAACC	C.ANG.AGCT	TCCCCTGCGC	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	



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FIG. 4C (Cont.)

	1101					1150
Bikunin	ACCG TCT G	GAGCTCCGGA	GATGACAAGG	AGCAGCTGG	TGAAGAAC	
R74593	ANCG.TCT.G	GAGCTTCGGA	GATGACAAGG	GNT		
R31730	ACCG.TCTGG	GAGCTCCGGA	GATGACAAGG	GAGCAGCTGG	GTGAAGAAC.	
R34701	ACCG.TCT.G	GAGCTCCGGA	GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.	
H02982	ACCG.TCTNG	GAGCTCCGGA	GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.	
R32676	ACCG.TCTGG	GAGCTCCGGA	GATGACAAGG	GAGCAGCTGG	.TGAAGAAC.	
T47439	ACCG.TCT.G	GAGCTCCGGA	GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.	
R73968	ACCG.TCT.G	GAGCTCCGGA	GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.	
H39840	ACCGGTCT.G	GAGCTCCGGA	GATGACAAGG	.AGCAGCTGG	.TGAAGAAC.	
H95233	
H39841	
N30199	ACCG.TCT.G	GAGCTCCGGA	GATNACAANG	.AGCAGCTGN	.TGAAGAACC	
T52966	
N29508	
N26919	
N26910	
H16757	
N27732	

	1151					1200
Bikunin	ACATATGT C	CTGT GACCG	CCCTGT CGC	C AAGAGG A	CT GGGGAA	
R31730	ACATATGTTC	CTGTTGACCG	NCCTGTTCGC	C.AAGAGG.A	TTGGGGGAA.	
R34701	ACATATGT.C	CTGT.GACCG	CCCTGT.CGC	C.AAGAGG.A	CT.GGGGAA.	
H02982	ACATATGT.C	CTGT.GACCG	NCCTGTTCGN	C.AAGAGG.A	CTNGGGGAAA	
R32676	ACATATGTTC	CTGTTGACCG	CCCTGTTCGC	C.AAGAGGGA	NTGGGGGAA.	
T47439	ACATATGT.C	CTGT.GACCG	CCCTGT.CGC	C.AAGAGG.A	CT.GGGGAA.	
R73968	ACATATGT.C	CTGT.GACCG	CCCTGT.CGC	C.AAGAGG.A	CT.GGGGAA.	
H39840	ACATATGT.C	CTGT.GACCG	CCCTGT.CGC	C.AAGAGG.A	CT.NGGGAA.	
H95233	
H39841C.	CCCTGT.CGC	CCAAAAGG.A	CT.GGGGAA.	
N30199	ACATATGT.C	CTGT.GACCG	CCCTNT.CGC	C.AAGAGG.A	CT.GGGNAAA	
T52966	
N29508CC.	CCCTNT.CGC	C.AAGAGG.A	CT.GGG.AA.	
N26919	
N26910	
H16757	
N27732	



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FIG. 4C (Cont.)

	1201					1250
Bikunin	GGGAGGGG	AGACTAT G	TGT GA GCT	TTTTTT	AA A	TAGA GG
R31730	.GGGAGGGG	A				
R34701	.GGGAGGGG.	AGACTAT.G.	TGT.GA.GCT	TTTTTT..AA	A.TA	
H02982	GGGAGGGG.	AGATTAT.G.	TGTTGA.GTT	TTTTTT..AA	ANTAG	
R32676	GGGAGGGGG	AGANTATTGT	TGTTGA.GNT	TTTTTTTAAA	ATTAGGAGGG	
T47439	.GGGAGGGG.	AGACTAT.G.	TGT.GA.GCT	TTTTTT..AA	A.TAGA..GG	
R73968	.GGGAGGGG.	AGACTAT.G.	TGT.GA.GCT	TTTTTT..AA	A.TAGA..GG	
H39840	.GGGAGGGG.	AGACTAT.G.	TGT.GA.GCT	TTTTTT..AA	A.TAGA..GG	
H95233
H39841	.GGGAGGGGA	AAACNAT.G.	TGT.GAACCT	TTTTTT.AAA	A.TAGA..GG	
N30199	.GGGAGGNG.	AGACTAT.G.	TGT.AA.GCT	TTTTTT..AA	A.TAGA..GG	
T52966
N29508	.GGGAGGGG.	AGACTA..G.	TGT.GA.GCT	TTTTTT..AA	A.TAGA..GG	
N26919
N26910
H16757
N27732
	1251					1300
Bikunin	GATTGACTC	GGATTTG A	GT GATC A	TTAGGG CT	GAGGTCTGTT	
R32676	GNTTGANTTC	GGGNTTTTNA	GTGATCCAT	TTAGGGGGNT	GAG	
T47439	GATTGACTC.	.GGATTTG.A	GT.GATC.A.	TTAGGG..CT	GAGGTCTNNT	
R73968	GATTGACTC.	.GGATTTG.A	GT.GATC.A.	TTAGGG..CT	GAGGTCTGTT	
H39840	GATTGACTC.	.GGATTTG.A	GT.GATC.A.	TTAGGG..CT	GAGGTCTGTT	
H95233A.	TTAGGG..CT	GAGGTCTGTT	
H39841	GATTGACTC.	.GGATTTG.A	GT.GATC.A.	TTAGGG..CT	GAGGTCTGTT	
N30199	GATTGACTC.	.GGATTTGGA	GT.GATC.A.	TTAGGG..CT	GAGGTCTGTT	
T52966
N29508	GATTGACTC.	.GGATTTG.A	GT.GATCNA.	TTAGGG..CT	GAGGTCTGTT	
N26919
N26910
H16757
N27732
	1301					1350
Bikunin	TCTCTGGGAG	GTAGGACGGC	TGCTTCC TG	G TC TGGCA	GGGATGGG	
T47439	TCTCTNGGAG	GTAGGACGA				
R73968	TCTCTGGGAG	GTAGGACGGC	TGCTTCC.TG	GGTCTTGGCA	.GGGATGGGG	
H39840	TCTCTGGGAG	GTAGGACGGC	TGCTTCC.TG	G.TC.TGGCA	.GGGATGGG.	
H95233	NCTCTGGGAG	NTAGGACGGC	TGCCTTCCTG	G.TC.TGGCA	.GGGATGGG.	
H39841	TCNCTGGGAG	GTAGGACGGC	TGCTCCCCTG	G.TC.TGGCA	.GGGATGGG.	
N30199	TCTCTGGGAG	GTAGGACGGC	TGCTTCC.TG	G.TC.TGGCA	.GGGATGGG.	
T52966TC.TGGCA	.GGGATGGG.	
N29508	TCTCTGGGAG	GTAGGACGGC	TGCTTCA.TG	G.TC.TGGCA	.GGGATGGG.	
N26919
N26910
H16757G	G.TC.TGGCA	.GGGATGGG.	
N27732CCCTG	GGTCCTGNCA	AGGNATGGGG	



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FIG. 4C (Cont.)

	1351		1400
Bikunin	TTTG CTTTG G AAATCCTC T AGGAGGCT CCTCCT CGC ATGG CC TG		
R73968	TTTG.CTTTG GGAAATCCTC TTNGGAGGCT CCTCCTTCGC ATGGGCCTTG		
H39840	TTTG.CTTTG GAGAATCCTC T.ANGAGGCT CCTCCT.CGC ATGG.CC.TG		
H95233	TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG		
H39841	TTTG.CTTTG G.AAANCCNC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG		
N30199	TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCTTCGC ATGG.CC.TG		
T52966	TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG		
N29508	TTTG.CTTTG G.AAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG		
N26919 GAGGCT CCTCCT.CGC ATGG.CC.TG		
N26910CTTTT GNAAATCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG		
H16757	TTTGCTTTTG G.AAANCCTC T.AGGAGGCT CCTCCT.CGC ATGG.CC.TG		
N27732	TTTG.CTTTG G.AAATCCTC TTAGGAGGCT CCTCCT.CGC ATGG.CC.TG		
	1401		1450
Bikunin	CAGT CT GG CAGCAG CCC CGAGTTGTTT CC TCGCTG ATC GATTTT		
R73968	CAGT.CTNGG CAGCANCCCC CGAGTTTTTT TCCTTCGCTG ATCCGATTTT		
H39840	CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTT		
H95233	CAGTTCT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTT		
H39841	CAGT.CT.GG CAGCAG.CCC CGAGTTGTTN .CC.TCGCTG ATC.GATNTC		
N30199	CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTT		
T52966	CAGT.CT.GG CAGCAG..CC CGAGTTGTTT .CC.TCGCTG ATC.GATTTT		
N29508	CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTT		
N26919	CAGT.CTTGG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTT		
N26910	CAGT.CT..G CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ATCGGATTTT		
H16757	CAGTNCT.GG CAGCAGACCC CGAGTTGTTT .CC.TCGCTG ATC.GATTTT		
N27732	CAGT.CT.GG CAGCAG.CCC CGAGTTGTTT .CC.TCGCTG ANC.GATTTT		
	1451		1500
Bikunin	TTT CCTCCA GGTAG AGT TTTC TTTG CTTATGTTGA ATTCCATTGC		
R73968	TTTTCTCCA GGTAAGAATT TTTCCTTT		
H39840	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
H95233	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
H39841	TTT.CCCCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ANTCCATTGC		
N30199	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
T52966	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
N29508	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
N26919	TTT.CCNCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
N26910	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		
H16757	TTTACCCCCA GGTAG..AGT TTTCCTTTGN CTTATGTTGA ATTCCATTGC		
N27732	TTT.CCTCCA GGTAG..AGT TTTC.TTTG. CTTATGTTGA ATTCCATTGC		



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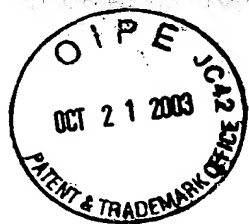
FIG. 4C (Cont.)

	1501					1550
Bikunin	CTCTTTT	CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT GT
H39840	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTTTGT
H95233	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
H39841	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
N30199	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
T52966	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
N29508	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
N26919	CTCTTTT	.CN	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
N26910	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
H16757	CTCTTTT	ACT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT
N27732	CTCTTTT	.CT	CATCACAGAA	GTGATGTTGG	AATCGTTTCT	TTTGTTT.GT

	1551					1600
Bikunin	CTGATTTATG	G	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
H39840	CTGATTTATG		GGTTTTTTTT	AAGTAT		
H95233	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
H39841	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
N30199	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
T52966	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
N29508	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
N26919	CTGATTTATG	G.	TTTTTTT	AAGTNTAAAC	AAAAGTTTTT	TATTAGCATT
N26910	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
H16757	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT
N27732	CTGATTTATG	G.	TTTTTTT	AAGTATAAAC	AAAAGTTTTT	TATTAGCATT

	1601					1650
Bikunin	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
H95233	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAA		
H39841	CTGAAAGAAG	GAAAGTAAAN	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
N30199	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
T52966	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
N29508	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
N26919	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
N26910	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
H16757	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	
N27732	CTGAAAGAAG	GAAAGTAAAA	TGTACAAGTT	TAATAAAAAAG	GGGCCTTCCC	

	1651					1689
Bikunin	CTTTAG	AAT	AAAAAAAAAA	AAAAAAAAAA	AAAAAAAAAA	
H39841	CTTTAA	.				
N30199	CTTTAG	.AAT	AAA			
T52966	CTTTAGGAAT		NAAAAA	AAAAA	AAGGGTG	
N29508	CTTTAG	.AAT	AAATTT	CAGC	ATGTGCTTTC	AA
N26919	CTTTAG	.AAT	AAAAAAAAAA	AAAAAAAAAA	A	
N26910	CTTTAG	.AAT	AAATTT	CAGC	ATGTGCTTTC	AAAAAA
H16757	CTTTAG	.AAT	AAAAAAAAAA	AAAAAAAAAA	AAAAAA	
N27732	CTTTAG	.AAT	AAAAAAAAAA	AAAAAAAAAA	AAAAAA	



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FIG. 4D

EST consensus MLRAEADGVS RLLGSLLLSG VLAADRERSI HDFCLVSKVV GRCRASMPRW 50
EST consensus WYNVTDGSCQ LFVYGGCDGN SNNYLTKEEC LKKCATVTEN ATGDLATSRN 100
EST consensus AADSSVPSAP RRQDSEDHSS DMFNYEEYCT ANAVTGPCRA SFPRWYFDVE 150
EST consensus RNSCNNFIYG GCRGNKNSYR SEEACMLRCF RQENPPLPL GSKVVVLAGL 200
EST consensus FVMVLILFLG ASMVYLIRVA RRNQERALRT VWSSGDDKEQ LVKNITYVL 248



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FIG. 4F

cDNA	GCACGAGTTG	GGAGGTGTAG	CGCGGCTCTG	AACGCGCTGA	GGGCCGTTGA	50
cDNA	GTGTCGCAGG	CGGCGAGGGC	GCGAGTGAGG	AGCAGACCCA	GGCATCGCGC	100
cDNA	GCCGAGAAGG	CCGGGCGTCC	CCACACTGAA	GGTCCGGAAA	GGCGACTTCC	150
cDNA	GGGGGCTTTG	GCACCTGGCG	GACCCTCCCG	GAGCGTCGGC	ACCTGAACGC	200
cDNA	GAGGCGCTCC	ATTGCGCGTG	CGCGTTGAGG	GGCTTCCCGC	ACCTGATCGC	250
cDNA	GAGACCCCAA	CGGCTGGTGG	CGTCGCCTGC	GCGTCTCGGC	TGAGCTGGCC	300
cDNA	ATGGCGCAGC	TGTGCGGGCT	GAGGCGGAGC	CGGGCGTTTC	TCGCCCTGCT	350
translation	M A Q L	C G L	R R S	R A F L	A L L	-11
cDNA	GGGATCGCTG	CTCCTCTCTG	GGGTCCTGGC	GGCCGACCGA	GAACGCAGCA	400
translation	G S L	L L S G	V L A	A D R	E R S I	7
cDNA	TCCACGACTT	CTGCCTGGTG	TCGAAGGTGG	TGGGCAGATG	CCGGGCCTCC	450
translation	H D F	C L V	S K V V	G R C	R A S	23
cDNA	ATGCCTAGGT	GGTGGTACAA	TGTCACTGAC	GGATCCTGCC	AGCTGTTTGT	500
translation	M P R W	W Y N	V T D	G S C Q	L F V	40
cDNA	GTATGGGGGC	TGTGACGGAA	ACAGCAATAA	TTACCTGACC	AAGGAGGAGT	550
translation	Y G G	C D G N	S N N	Y L T	K E E C	57
cDNA	GCCTCAAGAA	ATGTGCCACT	GTCACAGAGA	ATGCCACGGG	TGACCTGGCC	600
translation	L K K	C A T	V T E N	A T G	D L A	73
cDNA	ACCAGCAGGA	ATGCAGCGGA	TTCCTCTGTC	CCAAGTGCTC	CCAGAAGGCA	650
translation	T S R N	A A D	S S V	P S A P	R R Q	90
cDNA	GGATTCTGAA	GACCACTCCA	GCGATATGTT	CAACTATGAA	GAATACTGCA	700
translation	D S E	D H S S	D M F	N Y E	E Y C T	107
cDNA	CCGCCAACGC	AGTCACTGGG	CCTTGCCGTG	CATCCTTCCC	ACGCTGGTAC	750
translation	A N A	V T G	P C R A	S F P	R W Y	123
cDNA	TTTGACGTGG	AGAGGAACTC	CTGCAATAAC	TTCATCTATG	GAGGCTGCCG	800
translation	F D V E	R N S	C N N	F I Y G	G C R	140
cDNA	GGGCAATAAG	AACAGCTACC	GCTCTGAGGA	GGCCTGCATG	CTCCGCTGCT	850
translation	G N K	N S Y R	S E E	A C M	L R C F	157
cDNA	TCCGCCAGCA	GGAGAATCCT	CCCCTGCCCC	TTGGCTCAAA	GGTGGTGGTT	900
translation	R Q Q	E N P	P L P L	G S K	<u>V V V</u>	173
cDNA	CTGGCGGGGC	TGTTTCGTGAT	GGTGTGATC	CTCTTCCTGG	GAGCCTCCAT	950
translation	<u>L A G L</u>	<u>F V M</u>	<u>V L I</u>	<u>L F L G</u>	<u>A S M</u>	190
cDNA	GGTCTACCTG	ATCCGGGTGG	CACGGAGGAA	CCAGGAGCGT	GCCCTGCGCA	1000
translation	<u>V Y L</u>	<u>I R V A</u>	<u>R R N</u>	<u>Q E R</u>	<u>A L R T</u>	207
cDNA	CCGTCTGGAG	CTCCGGAGAT	GACAAGGAGC	AGCTGGTGAA	GAACACATAT	1050
translation	V W S	S G D	D K E Q	L V K	N T Y	223
cDNA	GTCCTGTGAC	CGCCCTGTCTG	CCAAGAGGAC	TGGGGAAGGG	AGGGGAGACT	1100
translation	V L	*				225

cDNA	CTGCGCACCG TCTGGAGCTT CGGAGATGA										782
translation	L	R	T	V	W	S	F	G	D		213

782
213



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FIG. 4F (Cont.)

cDNA	ATGTGTGAGC	TTTTTTTAAA	TAGAGGGATT	GA CTCGGATT	TGAGTGATCA	1150
cDNA	TTAGGGCTGA	GGTCTGTTTC	TCTGGGAGGT	AGGACGGCTG	CTTCCTGGTC	1200
cDNA	TGGCAGGGAT	GGGTTTGCTT	TGGAAATCCT	CTAGGAGGCT	CCTCCTCGCA	1250
cDNA	TGGCCTGCAG	TCTGGCAGCA	GCCCCGAGTT	GTTTCCTCGC	TGATCGATTT	1300
cDNA	CTTCCTCCA	GGTAGAGTTT	TCTTTGCTTA	TGTTGAATTC	CATTGCCTCC	1350
cDNA	TTTTCTCNAT	CACAGAAGTG	ATGTTGGAAT	CGTTTCTTTT	GTTTGTCTGA	1400
cDNA	TTTATGGTTT	TTTTAAGTAT	AAACAAAAGT	TTTTTATTAG	CATTCTGAAA	1450
cDNA	GAAGGAAAGT	AAAATGTACA	AGTTTAATAA	AAAGGGGCCT	TCCCCTTTAG	1500
cDNA	AATAAATTC	CAGCATGTTG	CTTTCAAAAA	AAAAAAAAAA	AAAA	1550

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FIG. 4G

EST consensus	MLR AEADGVSRL	GSLLLSGVLA	-1
PCR clone	MAQLCGL RRSRAFLALL	GSLLLSGVLA	-1
λcDNA clone	MAQLCGL RRSRAFLALL	GSLLLSGVLA	-1
EST consensus	ADRERSIHDF CLVSKVVGRC RASMPRWYN VTDGSCQLFV YGGCDGNSNN	50	
PCR clone	ADRERSIHDF CLVSKVVGRC RASMPRWYN VTDGSCQLFV YGGCDGNSNN	50	
λcDNA clone	ADRERSIHDF CLVSKVVGRC RASMPRWYN VTDGSCQLFV YGGCDGNSNN	50	
EST consensus	YLTKEECLKK CATVTENATG DLATSRNAAD SSVPSAPRRQ DSEDHSSDMF	100	
PCR clone	YLTKEECLKK CATVTENATG DLATSRNAAD SSVPSAPRRQ DSEDHSSDMF	100	
λcDNA clone	YLTKEECLKK CATVTENATG DLATSRNAAD SSVPSAPRRQ DSEDHSSDMF	100	
EST consensus	NYEEYCTANA VTGPCRASFP RWFYDVERNS CNNFIYGGCR GNKNSYRSEE	150	
PCR clone	NYEEYCTANA VTGPCRASFP RWFYDVERNS CNNFIYGGCR GNKNSYRSEE	150	
λcDNA clone	NYEEYCTANA VTGPCRASFP RWFYDVERNS CNNFIYGGCR GNKNSYRSEE	150	
EST consensus	ACMLRCFRQQ ENPPLPLGSK <u>VVVLAGLFVM VLILFLGASM VYLIRVARRN</u>	200	
PCR clone	ACMLRCFRQQ ENPPLPLGSK <u>VVVLAGLFVM VLILFLGASM VYLIRVARRN</u>	200	
λcDNA clone	ACMLRCFRQQ ENPPLPLGSK <u>VVVLAGLFVM VLILFLGASM VYLIRVARRN</u>	200	
EST consensus	QERALRTVWS SGDDKEQLVK NTYVL	225	
PCR clone	QERALRTVWS FGD	213	
λcDNA clone	QERALRTVWS SGDDKEQLVK NTYVL	225	

FIG. 5

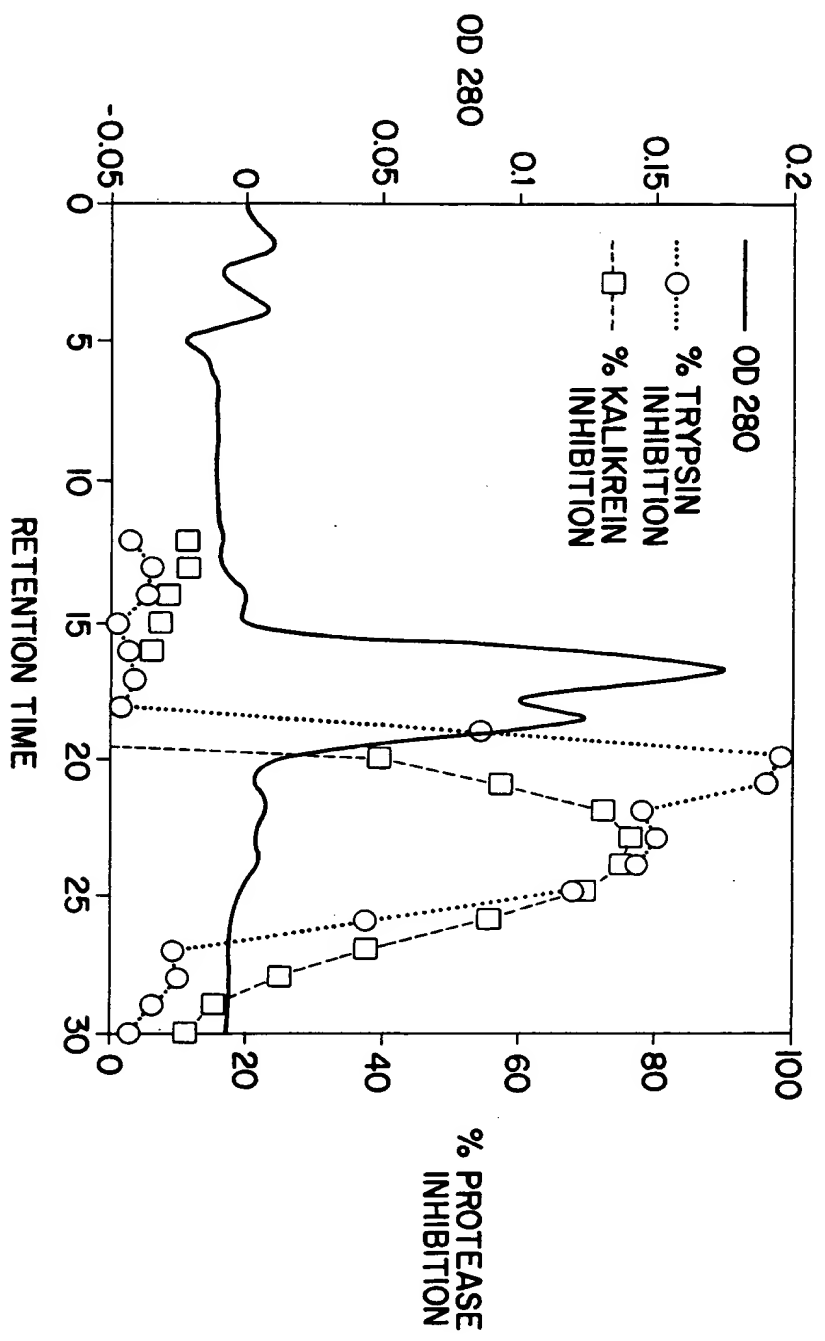
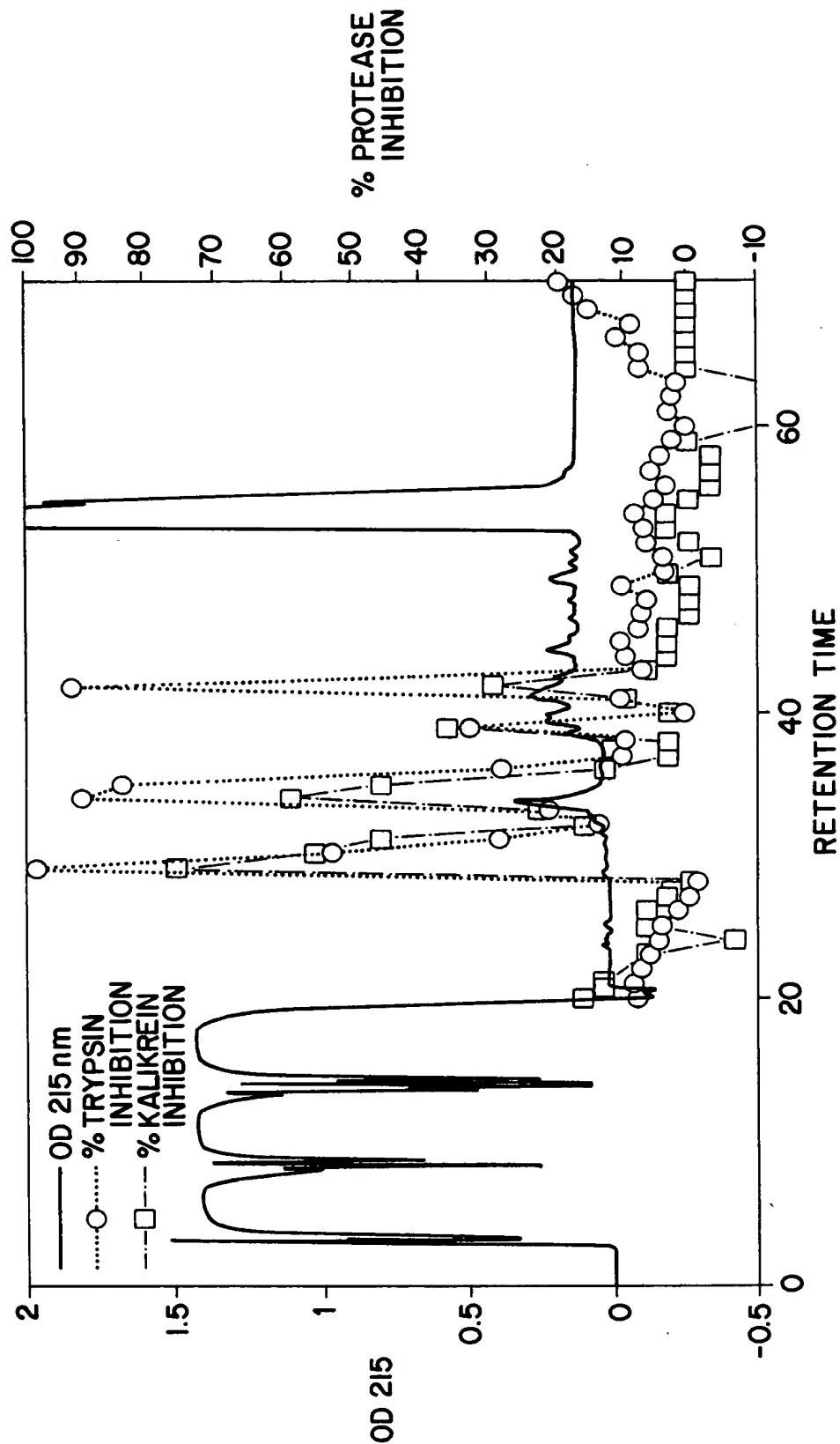


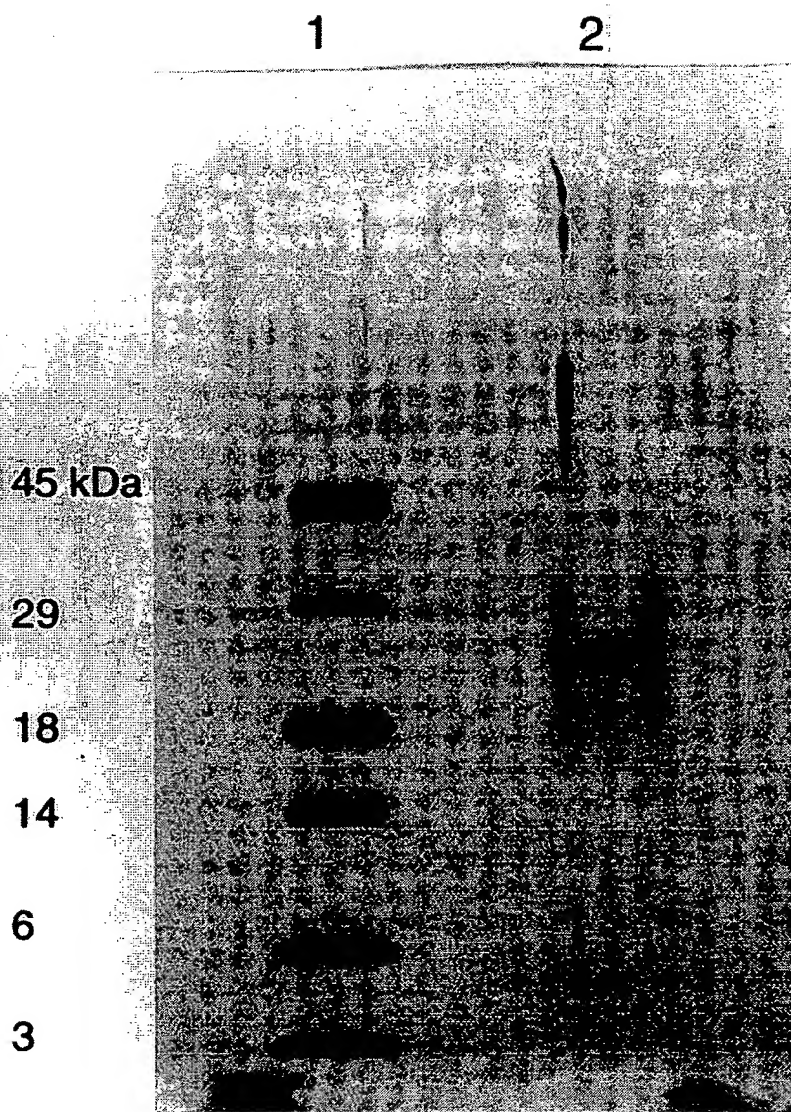
FIG. 6





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FIG. 7





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FIG. 8A

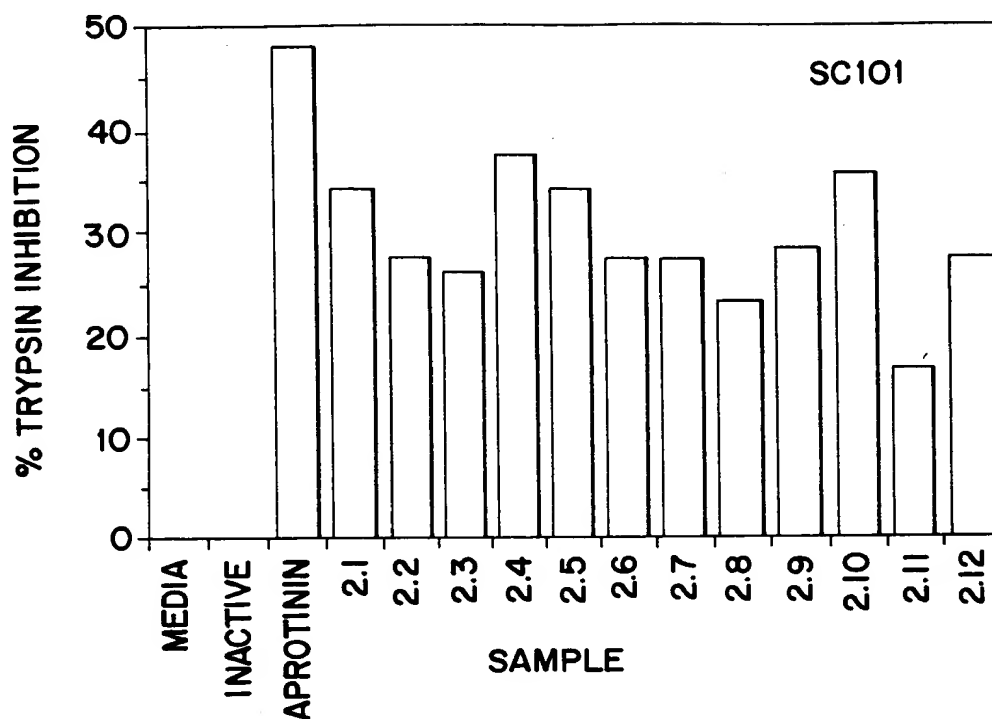


FIG. 8B

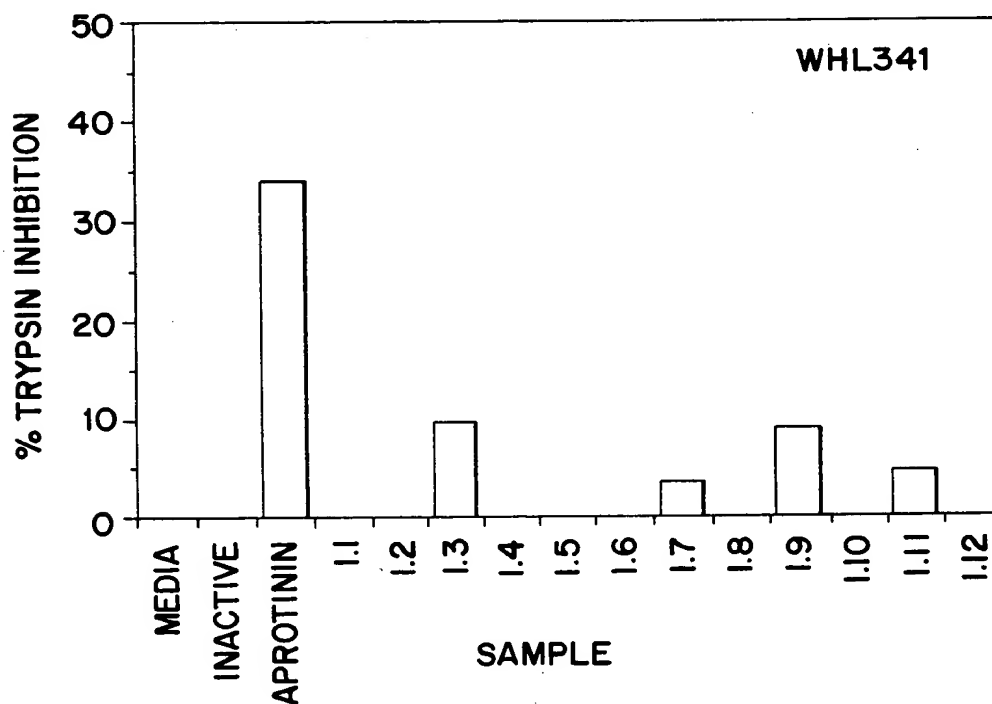


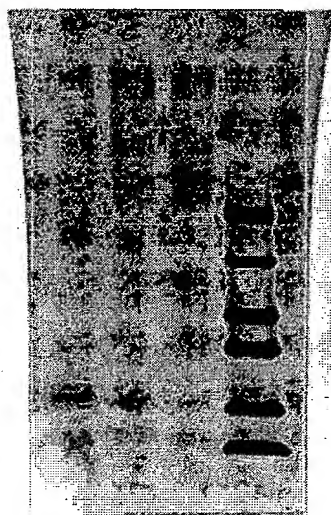
FIG. 9A

SDS-PAGE

Aprotinin

2.4

2.5



45 kDa
29
18
14
6
3

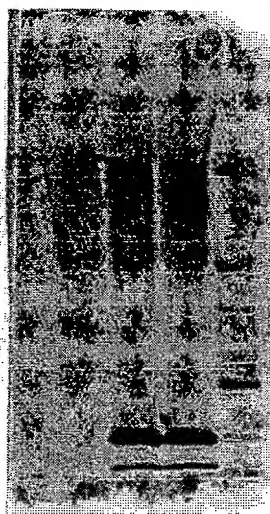
FIG. 9B

Western

Aprotinin

2.4

2.5



45 kDa
29
18
14
6
3

FIG. 10

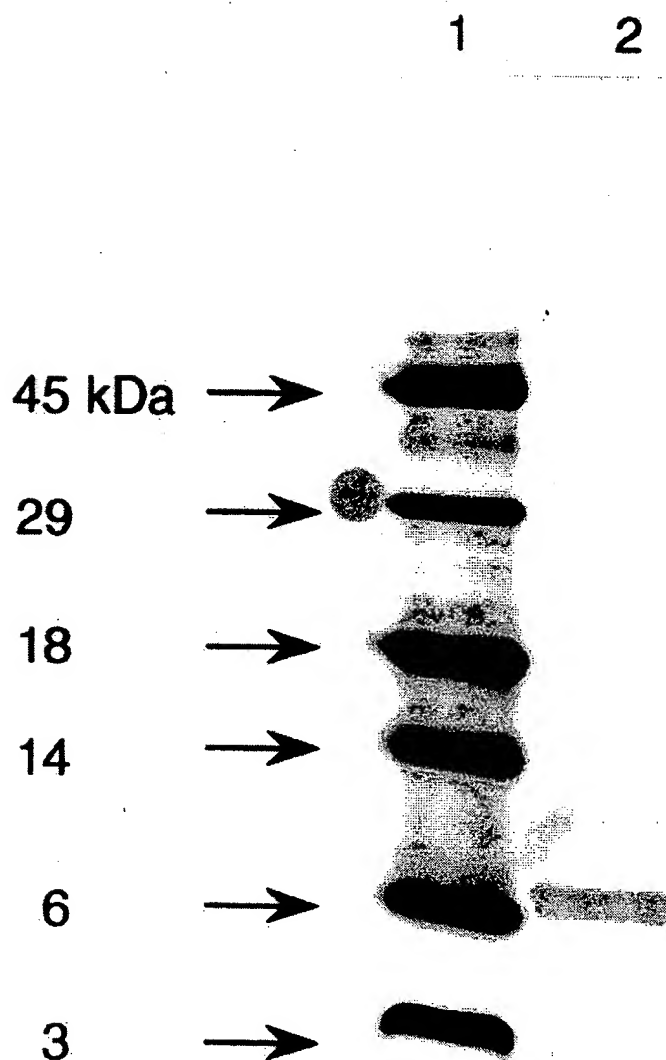


FIG. 11A

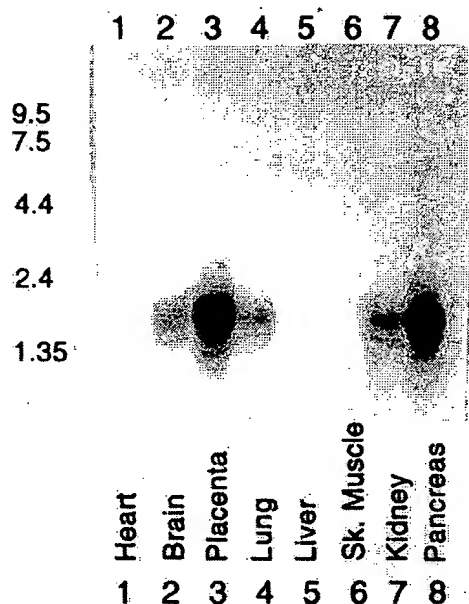


FIG. 11B

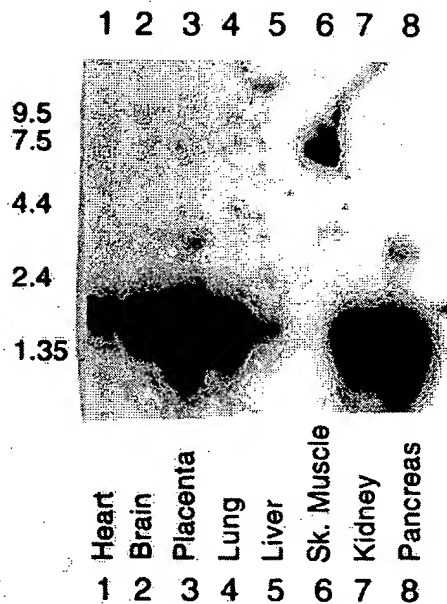


FIG. 12A

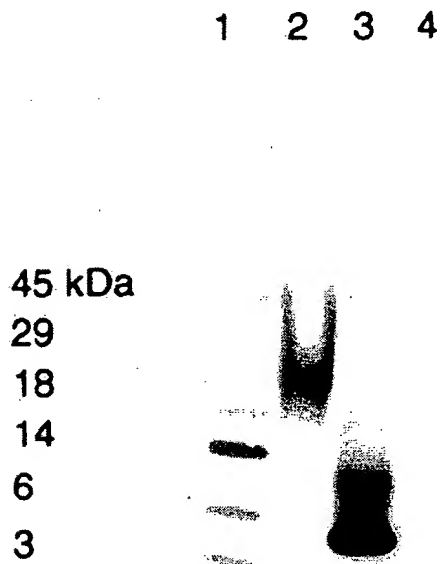
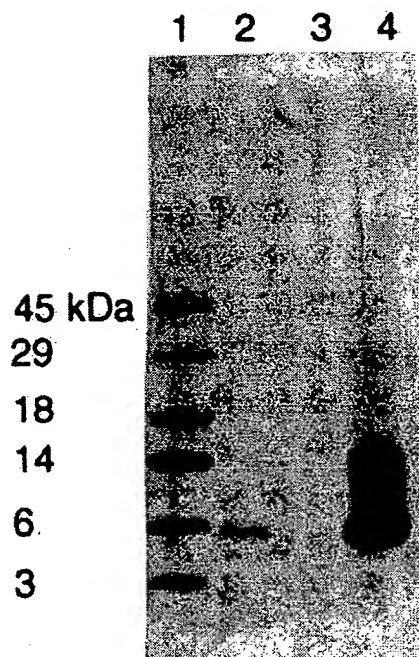


FIG. 12B





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FIG. 13

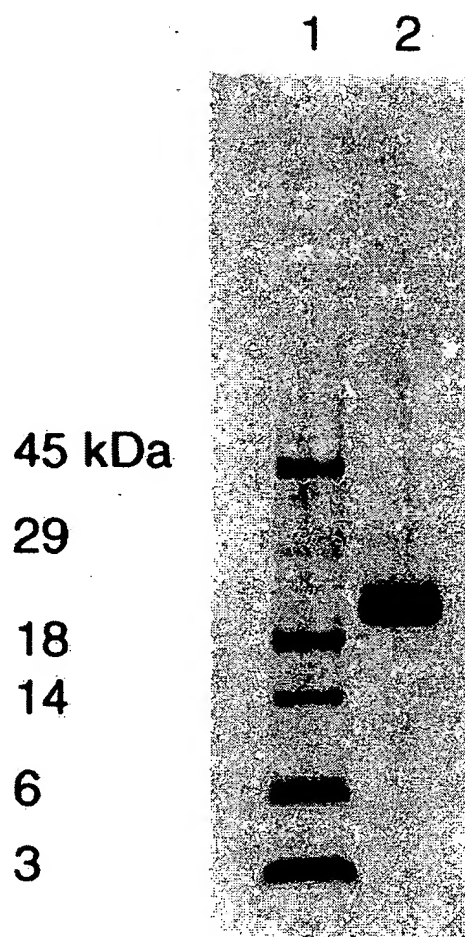


FIG. 14

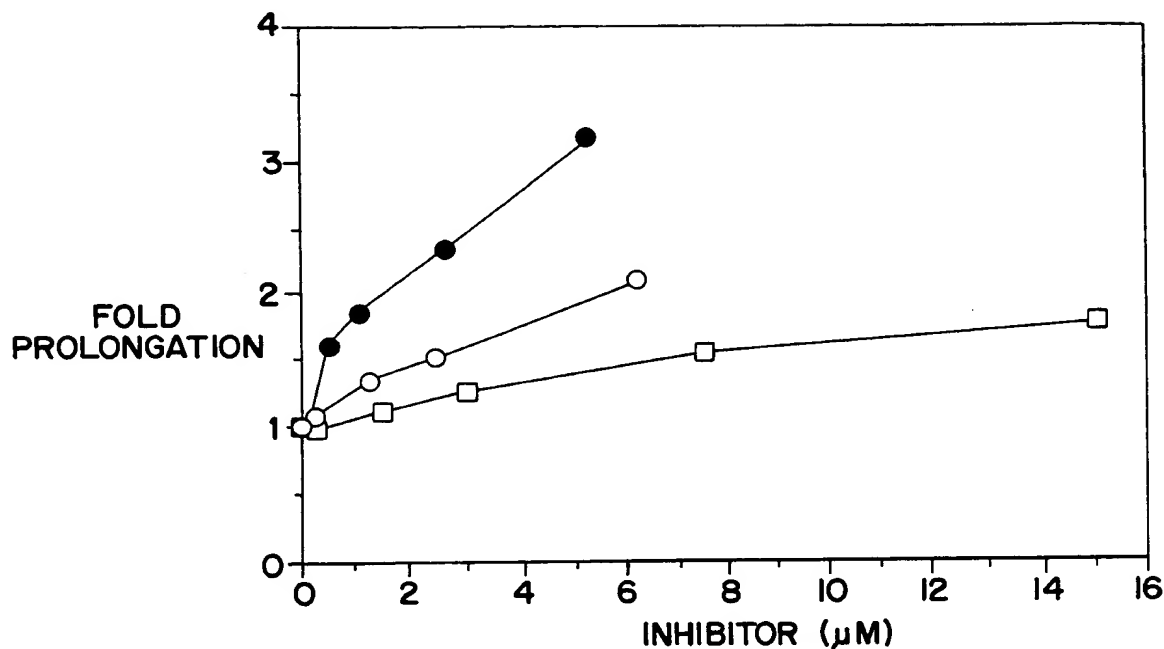


FIG. 15

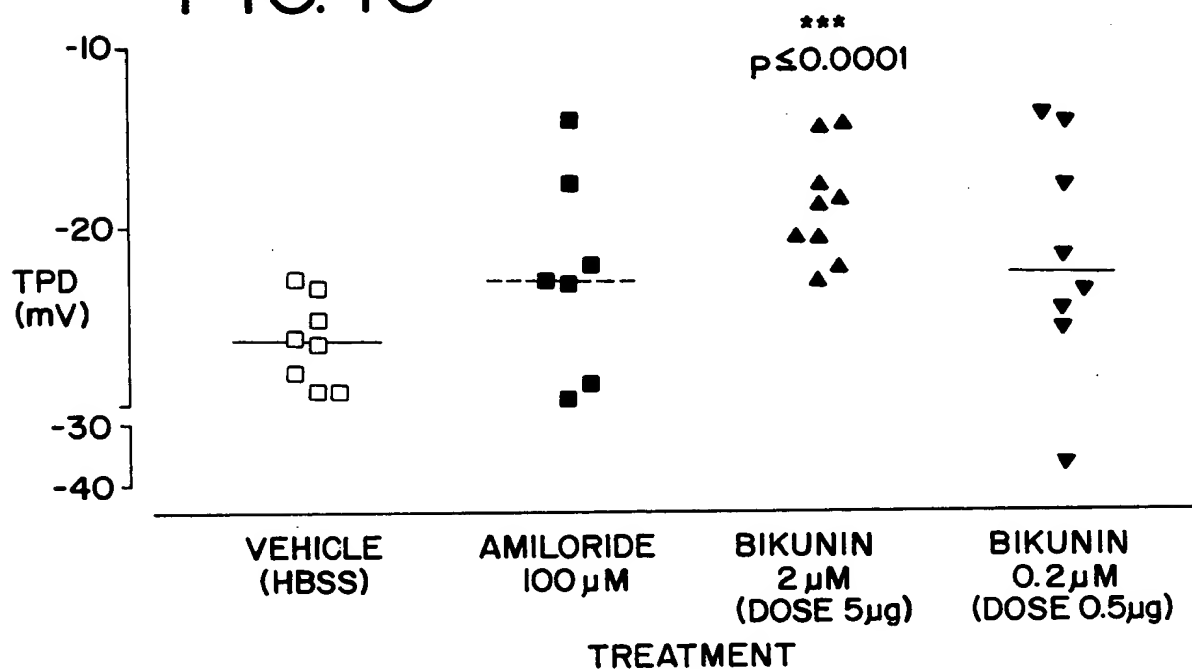


FIG. 16A

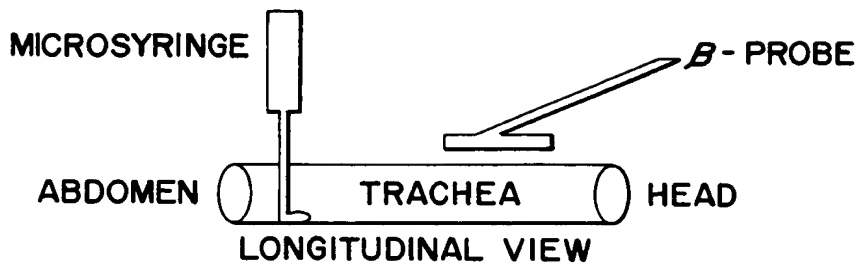


FIG. 16B

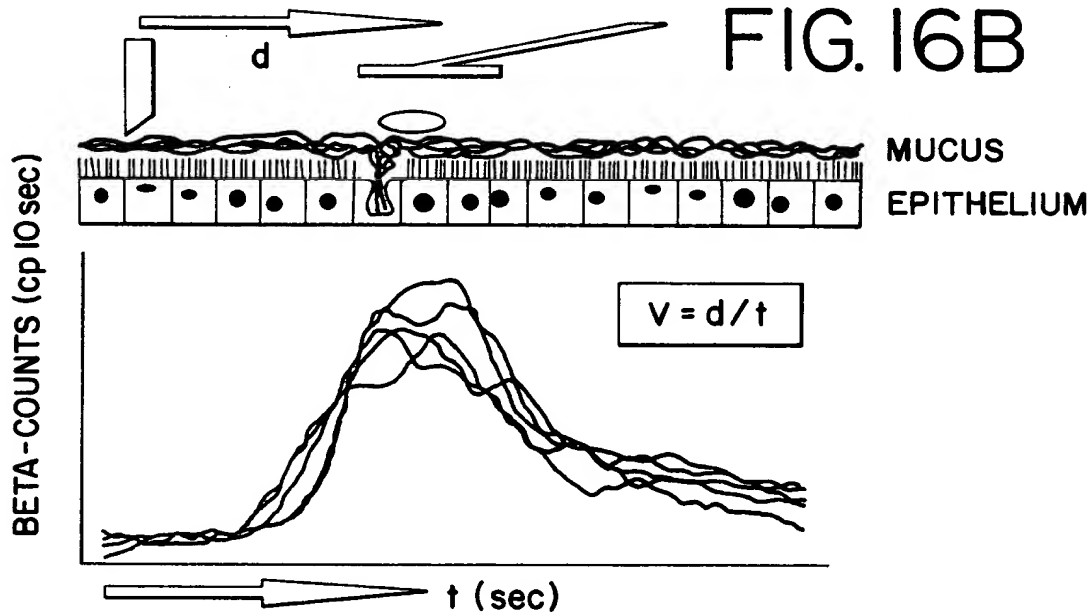


FIG. 17

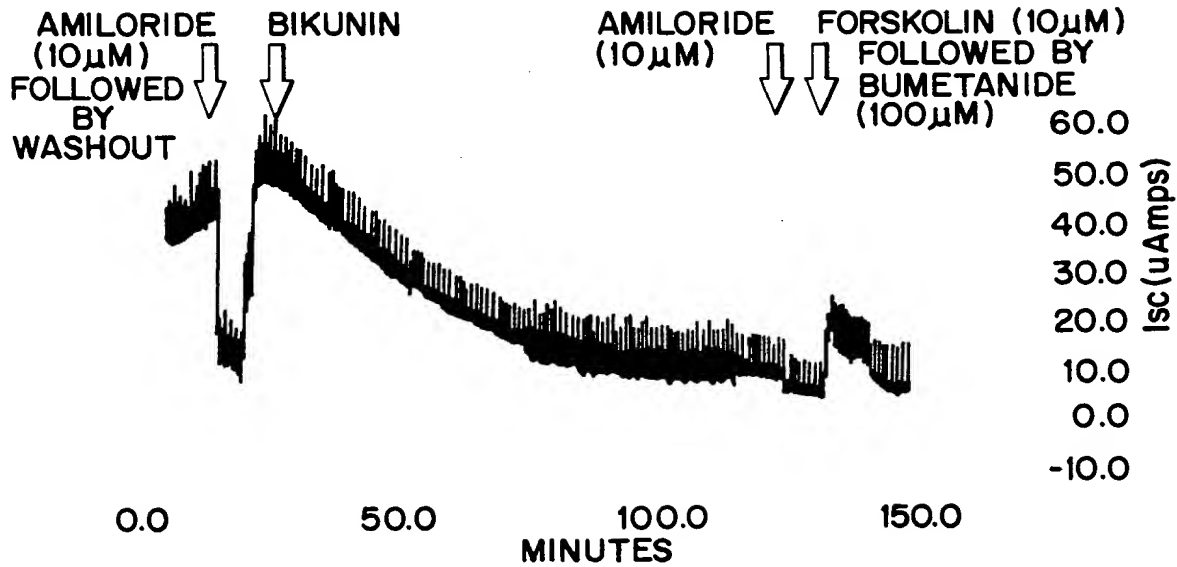


FIG. 18

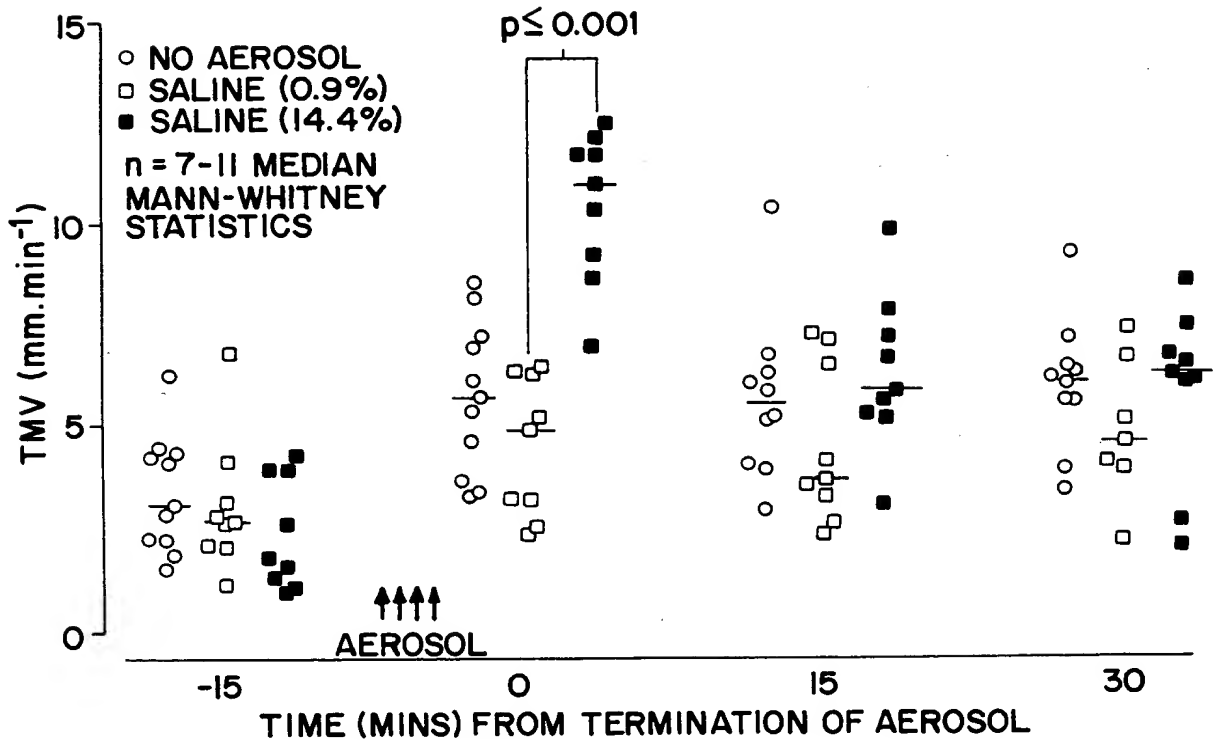


FIG. 19

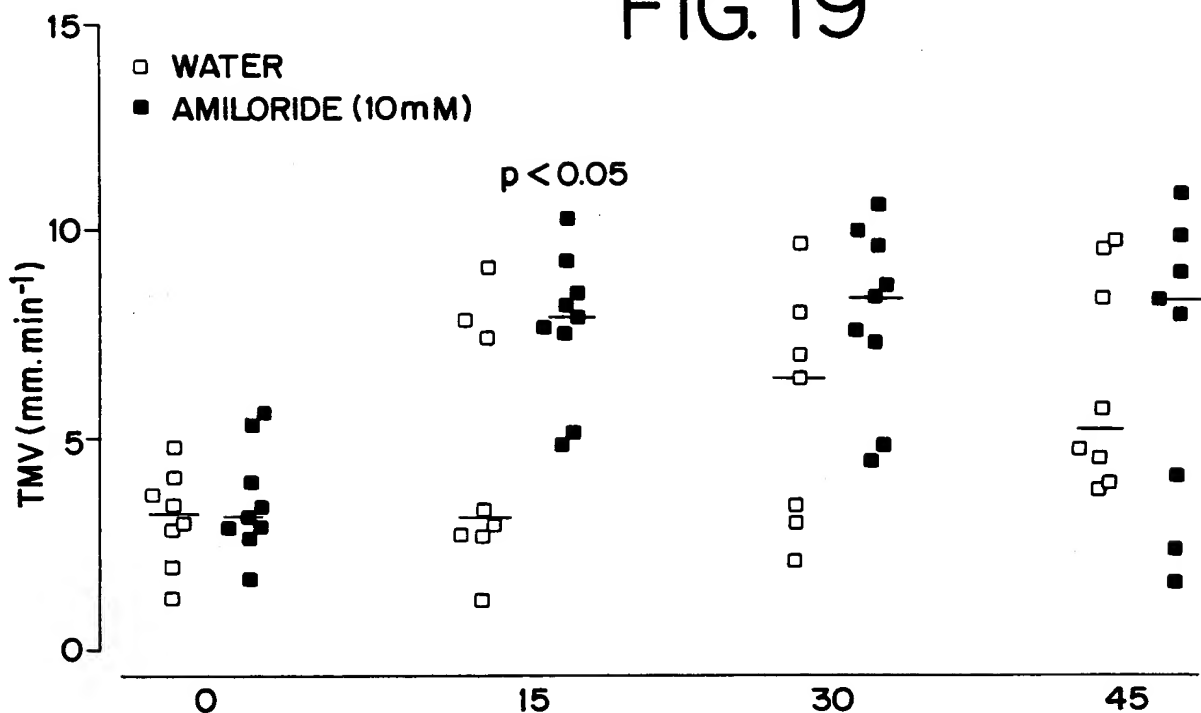


FIG. 20

